

Seq 18 10:2

Database : UniProt_02:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2680	100.0	507	2	Q9NQH7	Q9nqh7 homo sapien
2	2680	100.0	507	2	CAG30328	Cag30328 homo sapi
3	2676	99.9	507	2	Q6I9V9	Q6i9v9 homo sapien
4	2676	99.9	507	2	Q9BV27	Q9bv27 homo sapien
5	2676	99.9	507	2	CAG33677	Cag33677 homo sapi
6	2255	84.1	428	2	Q8NDA6	Q8nda6 homo sapien
7	1833	68.4	502	2	Q6DD23	Q6dd23 xenopus lae
8	1706.5	63.7	386	2	Q8BHT9	Q8bht9 mus musculu
9	1487	55.5	510	2	Q6NYT0	Q6nyt0 brachydanio
10	1487	55.5	510	2	AAH66473	Aah66473 brachydan
11	1393	52.0	278	2	Q9BVH0	Q9bvh0 homo sapien
12	895.5	33.4	513	2	Q7Q4S9	Q7q4s9 anopheles g
13	895	33.4	480	2	Q8GYQ0	Q8gyq0 arabidopsis
14	862	32.2	545	2	Q9W5W7	Q9w5w7 drosophila
15	821.5	30.7	451	2	Q9ZPZ5	Q9zpz5 arabidopsis

} for later date

RESULT 1

Q9NQH7

ID Q9NQH7 PRELIMINARY; PRT; 507 AA.
AC Q9NQH7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein LOC63929 (DJ1057D18.1 protein).
GN Name=LOC63929; Synonyms=dJ1057D18.1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Collins J.E., Huckle E.J.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Grinham J.A,
RA Cole C.G., Goward M.E., Aguado B., Mallya M., Mokrab Y., Huckle E.J.,
RA Beare D.M., Dunham I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL365514; CAB97210.1; -.
DR EMBL; BC004989; AAH04989.1; -.
DR EMBL; CR456442; CAG30328.1; -.
DR HSSP; P15034; 1A16.
DR MEROPS; M24.026; -.

DR GO; GO:0008235; F:metalloexopeptidase activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000994; Peptidase_M24.
 DR InterPro; IPR007865; Pept_M24B_N.
 DR Pfam; PF05195; AMP_N; 1.
 DR Pfam; PF00557; Peptidase_M24; 1.
 KW Hydrolase; Hypothetical protein.
 SQ SEQUENCE 507 AA; 57033 MW; 82D886736ABD0B5B CRC64;

Query Match 100.0%; Score 2680; DB 2; Length 507;
 Best Local Similarity 100.0%; Pred. No. 1.1e-192;
 Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MPWLLSAPKLVP	AVANVRGLSGCMLCSQRRYSLQVPERRIPNRYLGQPSPFTHPHLLRP	60
Db	1	MPWLLSAPKLVP	AVANVRGLSGCMLCSQRRYSLQVPERRIPNRYLGQPSPFTHPHLLRP	60
Qy	61	GEVTPGLSQVEYALRRHKLSLIQKEAQQSGTDQTVVVLSNPTYYSNDIPYTFHQDNN	120	
Db	61	GEVTPGLSQVEYALRRHKLSLIQKEAQQSGTDQTVVVLSNPTYYSNDIPYTFHQDNN	120	
Qy	121	FLYLCGFQEPDSILVLQSLPGKQLPSHKAILFVPRRDPSRELWDGPRSGTDGAIALTGVD	180	
Db	121	FLYLCGFQEPDSILVLQSLPGKQLPSHKAILFVPRRDPSRELWDGPRSGTDGAIALTGVD	180	
Qy	181	EAYTLEEFQHLLPKMKAETNMVWYDWMRPSHAQLHSDYMQPLTEAKAKSKNKVRGVQQLI	240	
Db	181	EAYTLEEFQHLLPKMKAETNMVWYDWMRPSHAQLHSDYMQPLTEAKAKSKNKVRGVQQLI	240	
Qy	241	QRLRLIKSPAIEIRMQIAGKLTSAFIETMFTSKAPVEEAFLYAKFEFECRARGADILAY	300	
Db	241	QRLRLIKSPAIEIRMQIAGKLTSAFIETMFTSKAPVEEAFLYAKFEFECRARGADILAY	300	
Qy	301	PPVVAGGNRSNTLHYVKNNQLIKDGEMVLLDGGCESSCYVSDITRTWPVNGRFTAPQAEL	360	
Db	301	PPVVAGGNRSNTLHYVKNNQLIKDGEMVLLDGGCESSCYVSDITRTWPVNGRFTAPQAEL	360	
Qy	361	YEAVLEIQRDCLALCFPGTSLENIYSMMLTLIGQKLKDLGIMKNIKENNAFKAARKYCPH	420	
Db	361	YEAVLEIQRDCLALCFPGTSLENIYSMMLTLIGQKLKDLGIMKNIKENNAFKAARKYCPH	420	
Qy	421	HVGHYLGMDVHDTDPDMPRSLPLQPGMVITIEPGIYIPEDDDKAPEKFRGLGVRIEDDVVV	480	
Db	421	HVGHYLGMDVHDTDPDMPRSLPLQPGMVITIEPGIYIPEDDDKAPEKFRGLGVRIEDDVVV	480	
Qy	481	TQDSPLILSADCPKEMNDIEQICSQAS	507	
Db	481	TQDSPLILSADCPKEMNDIEQICSQAS	507	

RESULT 2

RESULT 2

CAG30328

ID CAG30328 PRELIMINARY; PRT; 507 AA.
AC CAG30328;
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE DJ1057D18.1 protein.
GN DJ1057D18.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Grinham J.A,
RA Cole C.G., Goward M.E., Aguado B., Mallya M., Mokrab Y., Huckle E.J.,
RA Beare D.M., Dunham I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; CR456442; CAG30328.1; -.
SQ SEQUENCE 507 AA; 57033 MW; 82D886736ABD0B5B CRC64;

Query Match 100.0%; Score 2680; DB 2; Length 507;
Best Local Similarity 100.0%; Pred. No. 1.1e-192;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MPWLLSAPKLVP	AVANVRGLSGCMLCSQRRYS	LQPV	PERRIPNRYLGQPS	PFTHPHLLRP	60
Db	1	MPWLLSAPKLVP	AVANVRGLSGCMLCSQRRYS	LQPV	PERRIPNRYLGQPS	PFTHPHLLRP	60
Qy	61	GEVTPGLSQVEYALRRHK	LSLIQKEAQQSGTDQ	TVVVL	SNPTYYSNDIPYTF	HQDNN	120
Db	61	GEVTPGLSQVEYALRRHK	LSLIQKEAQQSGTDQ	TVVVL	SNPTYYSNDIPYTF	HQDNN	120
Qy	121	FLYLCGFQEPDSILVLQ	SLPGKQLPSHKAILFV	PRRDP	SRELWDGPRSGTDG	AIALTGV	180
Db	121	FLYLCGFQEPDSILVLQ	SLPGKQLPSHKAILFV	PRRDP	SRELWDGPRSGTDG	AIALTGV	180
Qy	181	EAYTLEEFQHLLPKMKA	ETNMVWYDWMRPSHAQL	HS	DYMQPLTEAKAKSKN	KV	240
Db	181	EAYTLEEFQHLLPKMKA	ETNMVWYDWMRPSHAQL	HS	DYMQPLTEAKAKSKN	KV	240
Qy	241	QRLRLIKSPA	EIERMQIAGKLTSQAFI	ETMFTSKAPVEEAFLY	AKFEFECRARGADIL	AY	300
Db	241	QRLRLIKSPA	EIERMQIAGKLTSQAFI	ETMFTSKAPVEEAFLY	AKFEFECRARGADIL	AY	300
Qy	301	PPVVAGGNRSNTLHYV	KNNQLIKD	GEMVLLDGGCESSCYV	SDITRTWPVNGRFTAP	Q	360
Db	301	PPVVAGGNRSNTLHYV	KNNQLIKD	GEMVLLDGGCESSCYV	SDITRTWPVNGRFTAP	Q	360
Qy	361	YEAVLEIQRDCLALCF	PGTSL	ENIYSMM	LT	LIGQKLKDLGIMKN	420
Db	361	YEAVLEIQRDCLALCF	PGTSL	ENIYSMM	LT	LIGQKLKDLGIMKN	420
Qy	421	HVGHYLGMDVHDT	PDMP	RS	LP	LQPGMVITIEPGIYIP	480
Db	421	HVGHYLGMDVHDT	PDMP	RS	LP	LQPGMVITIEPGIYIP	480

Qy 481 TQDSPLILSADCPKEMNDIEQICSQAS 507
| | | | | | | | | | | | | | | | | | | | | |
Db 481 TQDSPLILSADCPKEMNDIEQICSQAS 507

RESULT 3

Q6I9V9

ID Q6I9V9 PRELIMINARY; PRT; 507 AA.
AC Q6I9V9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LOC63929 protein.
GN Name=LOC63929;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; CR457396; CAG33677.1; -.
DR InterPro; IPR000994; Peptidase_M24.
DR InterPro; IPR007865; Pept_M24B_N.
DR Pfam; PF05195; AMP_N; 1.
DR Pfam; PF00557; Peptidase_M24; 1.
KW Hydrolase.
SQ SEQUENCE 507 AA; 57005 MW; CFA7DDA951AEA9DC CRC64;

Query Match 99.9%; Score 2676; DB 2; Length 507;
Best Local Similarity 99.8%; Pred. No. 2.2e-192;
Matches 506; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MPWLLSAPKLVP	AVANVRGLSGCMLCSQRRYS	LQVPERRIPNRYLGQPS	PFTPHLLRP	60
Db	1	MPWLLSAPKLVP	AVANVRGLSGCMLCSQRRYS	LQVPERRIPNRYLGQPS	PFTPHLLRP	60
Qy	61	GEVTPGLSQVEYALRRHKLMSLIQKEAQ	QSGTDQTVVVL	SNPTYYSNDIPYTFHQDNN		120
Db	61	GEVTPGLSQVEYALRRHKLMSLIQKEAQ	QSGTDQTVVVL	SNPTYYSNDIPYTFHQDNN		120
Qy	121	FLYL	CGFQEPDSILVLQSLPGKQLPSHKAILFVPRR	DPSRELWDGPRSGTDGAIALTGVD		180
Db	121	FLYL	CGFQEPDSILVLQSLPGKQLPSHKAILFVPRR	DPSRELWDGPRSGTDGAIALTGVD		180
Qy	181	EAYTLEEFQHLLPKMKAETNMVWYDWMRPSHAQLHSDYMQPLTEAKAKSKNKVRGVQQLI				240
Db	181	EAYTLEEFQHLLPKMKAETNMVWYDWMRPSHAQLHSDYMQPLTEAKAKSKNKVRGVQQLI				240
Qy	241	QRLRLIKSPAIEIRMQIAGKLTSQAFIETMFTSKAPVEEAFLYAKFEFECRARGADILAY				300
Db	241	QRLRLIKSPAIEIRMQIAGKLTSQAFIETMFTSKAPVEEAFLYAKFEFECRARGADILAY				300
Qy	301	PPVVAGGNRSNTLHYVKNNQLIKDGEMVLLDGGCESSCYVSDITRTWPVNGRFTAPQAEL				360
Db	301	PPVVAGGNRSNTLHYVKNNQLIKDGEMVLLDGGCESSCYASDITRTWPVNGRFTAPQAEL				360
Qy	361	YEAVLEIQRDCLALCFPGTSLENIYSMMLTLIGQKLKDLGIMKNIKENNAFKAARKYCPH				420
Db	361	YEAVLEIQRDCLALCFPGTSLENIYSMMLTLIGQKLKDLGIMKNIKENNAFKAARKYCPH				420

Qy	421	HVGHYLGMDVHDT	TPDM	PRSLPLQPGM	VITIEPGIYIPEDDKDAPEKFRGLGVRIEDDVVV	480
Db	421	HVGHYLGMDVHDT	TPDM	PRSLPLQPGM	VITIEPGIYIPEDDKDAPEKFRGLGVRIEDDVVV	480
Qy	481	TQDSPLILSADCPKEMNDIEQICSQAS				507
Db	481	TQDSPLILSADCPKEMNDIEQICSQAS				507

Database : PIR_79:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	821.5	30.7	451	2	A86226	hypothetical prote
2	745	27.8	511	2	S50581	hypothetical prote
3	722.5	27.0	486	2	T37572	probable metallopr
4	712	26.6	444	2	H82992	aminopeptidase P P
5	709	26.5	436	2	AB1840	aminopeptidase P [
6	705.5	26.3	430	2	B64096	X-Pro aminopeptida
7	680.5	25.4	446	2	F82609	aminopeptidase P X
8	644	24.0	441	2	S76440	hypothetical prote
9	635.5	23.7	438	2	AH0873	proline aminopepti
10	623.5	23.3	441	2	C91101	proline aminopepti
11	623.5	23.3	441	2	G85946	proline aminopepti
12	614.5	22.9	441	1	DPECP	X-Pro aminopeptida
13	598	22.3	437	2	AG0111	X-Pro aminopeptida
14	534	19.9	383	2	F87719	protein R119.2 [im
15	473	17.6	491	1	JN0491	X-Pro aminopeptida
16	424.5	15.8	535	2	S56261	probable membrane
17	415	15.5	493	2	A32454	X-Pro dipeptidase

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query					Description
No.	Score	Match	Length	DB	ID		
1	2680	100.0	507	9	US-09-780-016-2	Sequence 2, Appli	
2	2680	100.0	507	14	US-10-214-811-2	Sequence 2, Appli	
3	2680	100.0	507	16	US-10-766-074-2	Sequence 2, Appli	
4	2657.5	99.2	532	9	US-09-780-016-20	Sequence 20, Appl	
5	2657.5	99.2	532	14	US-10-214-811-20	Sequence 20, Appl	
6	2657.5	99.2	532	16	US-10-766-074-20	Sequence 20, Appl	
7	2558	95.4	484	9	US-09-780-016-26	Sequence 26, Appl	
8	2558	95.4	484	14	US-10-214-811-26	Sequence 26, Appl	
9	2558	95.4	484	16	US-10-766-074-26	Sequence 26, Appl	
10	2535.5	94.6	509	9	US-09-780-016-24	Sequence 24, Appl	
11	2535.5	94.6	509	14	US-10-214-811-24	Sequence 24, Appl	
12	2535.5	94.6	509	16	US-10-766-074-24	Sequence 24; Appl	

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	2680	100.0		507	4	US-09-780-016-2	Sequence 2, Appli
2	2680	100.0		507	4	US-10-214-811-2	Sequence 2, Appli
3	2657.5	99.2		532	4	US-09-780-016-20	Sequence 20, Appl
4	2657.5	99.2		532	4	US-10-214-811-20	Sequence 20, Appl
5	2558	95.4		484	4	US-09-780-016-26	Sequence 26, Appl
6	2558	95.4		484	4	US-10-214-811-26	Sequence 26, Appl
7	2535.5	94.6		509	4	US-09-780-016-24	Sequence 24, Appl
8	2535.5	94.6		509	4	US-10-214-811-24	Sequence 24, Appl
9	2255	84.1		428	4	US-09-780-016-22	Sequence 22, Appl
10	2255	84.1		428	4	US-10-214-811-22	Sequence 22, Appl

Database : A_Geneseq_23Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query			Description
	Score	Match	Length	DB	ID	
1	2680	100.0	507	4	AAE06717	Aae06717 Human nov
2	2657.5	99.2	532	4	AAE06726	Aae06726 Human nov
3	2558	95.4	484	4	AAE06729	Aae06729 Human nov
4	2535.5	94.6	509	4	AAE06728	Aae06728 Human nov
5	2532.5	94.5	515	7	ADE72525	Ade72525 Human end
6	2532.5	94.5	515	7	ADE72526	Ade72526 Human end
7	2255	84.1	428	4	AAE06727	Aae06727 Human nov
8	2255	84.1	428	5	ABP43879	Abp43879 Human pro
9	2232.5	83.3	453	4	AAE06725	Aae06725 Human nov
10	2126	79.3	408	4	AAM06839	Aam06839 Human foe
11	1887	70.4	371	8	ADJ71985	Adj71985 Human PMM
12	1494.5	55.8	298	4	ABG22568	Abg22568 Novel hum